



1600

RAW SEQUENCE LISTING

DATE: 04/21/2003

PATENT APPLICATION: US/09/250,083C

TIME: 15:09:39

Input Set : A:\seqlistcorrected.txt

Output Set: N:\CRF4\04212003\I250083C.raw

3 <110> APPLICANT: Dessen, Andrea
 4 Somers, William S.
 5 Stahl, Mark L.
 6 Seehra, Jasbir S.
 8 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF cPLA2, AND METHODS OF IDENTIFYING
 9 AGONISTS AND ANTAGONISTS USING SAME
 11 <130> FILE REFERENCE: GFN-5341
 13 <140> CURRENT APPLICATION NUMBER: 09/250,083C
 14 <141> CURRENT FILING DATE: 1999-02-15
 16 <160> NUMBER OF SEQ ID NOS: 3
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2247
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
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 32 1 5 10 15
 34 tcc cac aag ttt acg gta gtg gtg tta cgt gcc acc aaa gtg aca aag 96
 35 Ser His Lys Phe Thr Val Val Val Leu Arg Ala Thr Lys Val Thr Lys
 36 20 25 30
 38 ggg gcc ttt ggt gac atg ctt gat act cca gat ccc tat gtg gaa ctt 144
 39 Gly Ala Phe Gly Asp Met Leu Asp Thr Pro Asp Pro Tyr Val Glu Leu
 40 35 40 45
 42 ttt atc tct aca acc cct gac agc agg aag aga aca aga cat ttc aat 192
 43 Phe Ile Ser Thr Thr Pro Asp Ser Arg Lys Arg Thr Arg His Phe Asn
 44 50 55 60
 46 aat gac ata aac cct gtg tgg aat gag acc ttt gaa ttt att ttg gat 240
 47 Asn Asp Ile Asn Pro Val Trp Asn Glu Thr Phe Glu Phe Ile Leu Asp
 48 65 70 75 80
 50 cct aat cag gaa aat gtt ttg gag att acg tta atg gat gcc aat tat 288
 51 Pro Asn Gln Glu Asn Val Leu Glu Ile Thr Leu Met Asp Ala Asn Tyr
 52 85 90 95
 54 gtc atg gat gaa act cta ggg aca gca aca ttt act gta tct tct atg 336
 55 Val Met Asp Glu Thr Leu Gly Thr Ala Thr Phe Thr Val Ser Ser Met
 56 100 105 110
 58 aag gtg gga gaa aag aaa gaa gtt cct ttt att ttc aac caa gtc act 384
 59 Lys Val Gly Glu Lys Lys Glu Val Pro Phe Ile Phe Asn Gln Val Thr
 60 115 120 125

ENTERED

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62 gaa atg gtt cta gaa atg tct ctt gaa gtt tgc tca tgc cca gac cta 432
63 Glu Met Val Leu Glu Met Ser Leu Glu Val Cys Ser Cys Pro Asp Leu
64 130 135 140
66 cga ttt agt atg gct ctg tgt gat cag gag aag act ttc aga caa cag 480
67 Arg Phe Ser Met Ala Leu Cys Asp Gln Glu Lys Thr Phe Arg Gln Gln
68 145 150 155 160
70 aga aaa gaa cac ata agg gag agc atg aag aaa ctc ttg ggt cca aag 528
71 Arg Lys Glu His Ile Arg Glu Ser Met Lys Lys Leu Leu Gly Pro Lys
72 165 170 175
74 aat agt gaa gga ttg cat tct gca cgt gat gtg cct gtg gta gcc ata 576
75 Asn Ser Glu Gly Leu His Ser Ala Arg Asp Val Pro Val Val Ala Ile
76 180 185 190
78 ttg ggt tca ggt ggg ggt ttc cga gcc atg gtg gga ttc tct ggt gtg 624
79 Leu Gly Ser Gly Gly Gly Phe Arg Ala Met Val Gly Phe Ser Gly Val
80 195 200 205
82 atg aag gca tta tac gaa tca gga att ctg gat tgt gct acc tac gtt 672
83 Met Lys Ala Leu Tyr Glu Ser Gly Ile Leu Asp Cys Ala Thr Tyr Val
84 210 215 220
86 gct ggt ctt tct ggc tcc acc tgg tat atg tca acc ttg tat tct cac 720
87 Ala Gly Leu Ser Gly Ser Thr Trp Tyr Met Ser Thr Leu Tyr Ser His
88 225 230 235 240
90 cct gat ttt cca gag aaa ggg cca gag gag att aat gaa gaa cta atg 768
91 Pro Asp Phe Pro Glu Lys Gly Pro Glu Glu Ile Asn Glu Glu Leu Met
92 245 250 255
94 aaa aat gtt agc cac aat ccc ctt tta ctt ctc aca cca cag aaa gtt 816
95 Lys Asn Val Ser His Asn Pro Leu Leu Leu Leu Thr Pro Gln Lys Val
96 260 265 270
98 aaa aga tat gtt gag tct tta tgg aag aag aaa agc tct gga caa cct 864
99 Lys Arg Tyr Val Glu Ser Leu Trp Lys Lys Lys Ser Ser Gly Gln Pro
100 275 280 285
102 gtc acc ttt act gat atc ttt ggg atg tta ata gga gaa aca cta att 912
103 Val Thr Phe Thr Asp Ile Phe Gly Met Leu Ile Gly Glu Thr Leu Ile
104 290 295 300
106 cat aat aga atg aat act act ctg agc agt ttg aag gaa aaa gtt aat 960
107 His Asn Arg Met Asn Thr Thr Leu Ser Ser Leu Lys Glu Lys Val Asn
108 305 310 315 320
110 act gca caa tgc cct tta cct ctt ttc acc tgt ctt cat gtc aaa cct 1008
111 Thr Ala Gln Cys Pro Leu Pro Leu Phe Thr Cys Leu His Val Lys Pro
112 325 330 335
114 gac gtt tca gag ctg atg ttt gca gat tgg gtt gaa ttt agt cca tac 1056
115 Asp Val Ser Glu Leu Met Phe Ala Asp Trp Val Glu Phe Ser Pro Tyr
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118 gaa att ggc atg gct aaa tat ggt act ttt atg gct ccc gac tta ttt 1104
119 Glu Ile Gly Met Ala Lys Tyr Gly Thr Phe Met Ala Pro Asp Leu Phe
120 355 360 365
122 gga agc aaa ttt ttt atg gga aca gtc gtt aag aag tat gaa gaa aac 1152
123 Gly Ser Lys Phe Phe Met Gly Thr Val Val Lys Lys Tyr Glu Glu Asn
124 370 375 380
126 ccc ttg cat ttc tta atg ggt gtc tgg ggc agt gcc ttt tcc ata ttg 1200

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130 ttc aac aga gtt ttg ggc gtt tct ggt tca caa agc aga ggc tcc aca 1248
131 Phe Asn Arg Val Leu Gly Val Ser Gly Ser Gln Ser Arg Gly Ser Thr
132 405 410 415
134 atg gag gaa gaa tta gaa aat att acc aca aag cat att gtg agt aat 1296
135 Met Glu Glu Glu Leu Glu Asn Ile Thr Thr Lys His Ile Val Ser Asn
136 420 425 430
138 gat agc tcg gac agt gat gat gaa tca cac gaa ccc aaa ggc act gaa 1344
139 Asp Ser Ser Asp Ser Asp Asp Glu Ser His Glu Pro Lys Gly Thr Glu
140 435 440 445
142 aat gaa gat gct gga agt gac tat caa agt gat aat caa gca agt tgg 1392
143 Asn Glu Asp Ala Gly Ser Asp Tyr Gln Ser Asp Asn Gln Ala Ser Trp
144 450 455 460
146 att cat cgt atg ata atg gcc ttg gtg agt gat tca gct tta ttc aat 1440
147 Ile His Arg Met Ile Met Ala Leu Val Ser Asp Ser Ala Leu Phe Asn
148 465 470 475 480
150 acc aga gaa gga cgt gct ggg aag gta cac aac ttc atg ctg ggc ttg 1488
151 Thr Arg Glu Gly Arg Ala Gly Lys Val His Asn Phe Met Leu Gly Leu
152 485 490 495
154 aat ctc aat aca tct tat cca ctg tct cct ttg agt gac ttt gcc aca 1536
155 Asn Leu Asn Thr Ser Tyr Pro Leu Ser Pro Leu Ser Asp Phe Ala Thr
156 500 505 510
158 cag gac tcc ttt gat gat gat gaa ctg gat gca gct gta gca gat cct 1584
159 Gln Asp Ser Phe Asp Asp Asp Glu Leu Asp Ala Ala Val Ala Asp Pro
160 515 520 525
162 gat gaa ttt gag cga ata tat gag cct ctg gat gtc aaa agt aaa aag 1632
163 Asp Glu Phe Glu Arg Ile Tyr Glu Pro Leu Asp Val Lys Ser Lys Lys
164 530 535 540
166 att cat gta gtg gac agt ggg ctc aca ttt aac ctg ccg tat ccc ttg 1680
167 Ile His Val Val Asp Ser Gly Leu Thr Phe Asn Leu Pro Tyr Pro Leu
168 545 550 555 560
170 ata ctg aga cct cag aga ggg gtt gat ctc ata atc tcc ttt gac ttt 1728
171 Ile Leu Arg Pro Gln Arg Gly Val Asp Leu Ile Ile Ser Phe Asp Phe
172 565 570 575
174 tct gca agg cca agt gac tct agt cct ccg ttc aag gaa ctt cta ctt 1776
175 Ser Ala Arg Pro Ser Asp Ser Ser Pro Pro Phe Lys Glu Leu Leu Leu
176 580 585 590
178 gca gaa aag tgg gct aaa atg aac aag ctc ccc ttt cca aag att gat 1824
179 Ala Glu Lys Trp Ala Lys Met Asn Lys Leu Pro Phe Pro Lys Ile Asp
180 595 600 605
182 cct tat gtg ttt gat cgg gaa ggg ctg aag gag tgc tat gtc ttt aaa 1872
183 Pro Tyr Val Phe Asp Arg Glu Gly Leu Lys Glu Cys Tyr Val Phe Lys
184 610 615 620
186 ccc aag aat cct gat atg gag aaa gat tgc cca acc atc atc cac ttt 1920
187 Pro Lys Asn Pro Asp Met Glu Lys Asp Cys Pro Thr Ile Ile His Phe
188 625 630 635 640
190 gtt ctg gcc aac atc aac ttc aga aag tac aag gct cca ggt gtt cca 1968
191 Val Leu Ala Asn Ile Asn Phe Arg Lys Tyr Lys Ala Pro Gly Val Pro

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194 agg gaa act gag gaa gag aaa gaa atc gct gac ttt gat att ttt gat 2016
195 Arg Glu Thr Glu Glu Glu Lys Glu Ile Ala Asp Phe Asp Ile Phe Asp
196          660          665          670
198 gac cca gaa tca cca ttt tca acc ttc aat ttt caa tat cca aat caa 2064
199 Asp Pro Glu Ser Pro Phe Ser Thr Phe Asn Phe Gln Tyr Pro Asn Gln
200          675          680          685
202 gca ttc aaa aga cta cat gat ctt atg cac ttc aat act ctg aac aac 2112
203 Ala Phe Lys Arg Leu His Asp Leu Met His Phe Asn Thr Leu Asn Asn
204          690          695          700
206 att gat gtg ata aaa gaa gcc atg gtt gaa agc att gaa tat aga aga 2160
207 Ile Asp Val Ile Lys Glu Ala Met Val Glu Ser Ile Glu Tyr Arg Arg
208 705          710          715          720
210 cag aat cca tct cgt tgc tct gtt tcc ctt agt aat gtt gag gca aga 2208
211 Gln Asn Pro Ser Arg Cys Ser Val Ser Leu Ser Asn Val Glu Ala Arg
212          725          730          735
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231 Gly Ala Phe Gly Asp Met Leu Asp Thr Pro Asp Pro Tyr Val Glu Leu
232 35 40 45
234 Phe Ile Ser Thr Thr Pro Asp Ser Arg Lys Arg Thr Arg His Phe Asn
235 50 55 60
237 Asn Asp Ile Asn Pro Val Trp Asn Glu Thr Phe Glu Phe Ile Leu Asp
238 65 70 75 80
240 Pro Asn Gln Glu Asn Val Leu Glu Ile Thr Leu Met Asp Ala Asn Tyr
241 85 90 95
243 Val Met Asp Glu Thr Leu Gly Thr Ala Thr Phe Thr Val Ser Ser Met
244 100 105 110
246 Lys Val Gly Glu Lys Lys Glu Val Pro Phe Ile Phe Asn Gln Val Thr
247 115 120 125
249 Glu Met Val Leu Glu Met Ser Leu Glu Val Cys Ser Cys Pro Asp Leu
250 130 135 140
252 Arg Phe Ser Met Ala Leu Cys Asp Gln Glu Lys Thr Phe Arg Gln Gln
253 145 150 155 160
255 Arg Lys Glu His Ile Arg Glu Ser Met Lys Lys Leu Leu Gly Pro Lys
256 165 170 175
258 Asn Ser Glu Gly Leu His Ser Ala Arg Asp Val Pro Val Val Ala Ile
259 180 185 190
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267 Ala Gly Leu Ser Gly Ser Thr Trp Tyr Met Ser Thr Leu Tyr Ser His			
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270 Pro Asp Phe Pro Glu Lys Gly Pro Glu Glu Ile Asn Glu Glu Leu Met			
271 245	250	255	
273 Lys Asn Val Ser His Asn Pro Leu Leu Leu Leu Thr Pro Gln Lys Val			
274 260	265	270	
276 Lys Arg Tyr Val Glu Ser Leu Trp Lys Lys Lys Ser Ser Gly Gln Pro			
277 275	280	285	
279 Val Thr Phe Thr Asp Ile Phe Gly Met Leu Ile Gly Glu Thr Leu Ile			
280 290	295	300	
282 His Asn Arg Met Asn Thr Thr Leu Ser Ser Leu Lys Glu Lys Val Asn			
283 305	310	315	320
285 Thr Ala Gln Cys Pro Leu Pro Leu Phe Thr Cys Leu His Val Lys Pro			
286 325	330	335	
288 Asp Val Ser Glu Leu Met Phe Ala Asp Trp Val Glu Phe Ser Pro Tyr			
289 340	345	350	
291 Glu Ile Gly Met Ala Lys Tyr Gly Thr Phe Met Ala Pro Asp Leu Phe			
292 355	360	365	
294 Gly Ser Lys Phe Phe Met Gly Thr Val Val Lys Lys Tyr Glu Glu Asn			
295 370	375	380	
297 Pro Leu His Phe Leu Met Gly Val Trp Gly Ser Ala Phe Ser Ile Leu			
298 385	390	395	400
300 Phe Asn Arg Val Leu Gly Val Ser Gly Ser Gln Ser Arg Gly Ser Thr			
301 405	410	415	
303 Met Glu Glu Glu Leu Glu Asn Ile Thr Thr Lys His Ile Val Ser Asn			
304 420	425	430	
306 Asp Ser Ser Asp Ser Asp Asp Glu Ser His Glu Pro Lys Gly Thr Glu			
307 435	440	445	
309 Asn Glu Asp Ala Gly Ser Asp Tyr Gln Ser Asp Asn Gln Ala Ser Trp			
310 450	455	460	
312 Ile His Arg Met Ile Met Ala Leu Val Ser Asp Ser Ala Leu Phe Asn			
313 465	470	475	480
315 Thr Arg Glu Gly Arg Ala Gly Lys Val His Asn Phe Met Leu Gly Leu			
316 485	490	495	
318 Asn Leu Asn Thr Ser Tyr Pro Leu Ser Pro Leu Ser Asp Phe Ala Thr			
319 500	505	510	
321 Gln Asp Ser Phe Asp Asp Asp Glu Leu Asp Ala Ala Val Ala Asp Pro			
322 515	520	525	
324 Asp Glu Phe Glu Arg Ile Tyr Glu Pro Leu Asp Val Lys Ser Lys Lys			
325 530	535	540	
327 Ile His Val Val Asp Ser Gly Leu Thr Phe Asn Leu Pro Tyr Pro Leu			
328 545	550	555	560
330 Ile Leu Arg Pro Gln Arg Gly Val Asp Leu Ile Ile Ser Phe Asp Phe			
331 565	570	575	
333 Ser Ala Arg Pro Ser Asp Ser Ser Pro Phe Lys Glu Leu Leu Leu			
334 580	585	590	

VERIFICATION SUMMARY

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